

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/421, 106ASource: 1600Date Processed by STIC: 1/9/2003

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JAN 2 1 2003

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual/- ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
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 U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

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Revised 01/29/2002

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JAN 2 1 2003



1600

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

2 <1105 AFFLICANT: Byram, Joseph R.

FATENT APPLICATION: US/09/421,106A

DATE: 01/09/2003

TIME: 10:55:57

Input Set : D:\SoyBac.txt

Output Set: N:\CRF4\01092003\I421106A.raw

PLANTS pr 1-7 7 <130 FILE REFERENCE: 38-21(15598)B 3 <140 CURRENT APPLICATION NUMBER: 09/421,106A 10 <141 CURRENT FILING DATE: 1999-10-15 12 - 150 NUMBER OF SEQ ID NOS: 36938 Does Not Comply Corrected Diskette Needed ERRORED SEQUENCES 14 - 210 SEO ID NO: 3 TYPE: DIA ORGANISM: C.ycine max 19 CONT OTHER INFORMATION: unsure at all n locations E--> 20 <400> SEQUENCE: 1 22 actcattage ttatggagaa gettttett tttaactnte tteteetatt agagettata 24 quasagetta temasamaan geceactata tatteteeaa teteeteete teeceatatat > 26 ategateete gotttegaca titiggat > 51 -00100 SEP ID ID: -52 -00110 SENGTE: 423 Sa -00120 TYPE: DNA 84 KR13F OF GANISH: Glycine max) 22207 36 - 123 OTHER INFORMATION: unsure at all n locations E--> 57 <400> SEQUENCE: 3 59 myotigtgig ttgtgag.gy lagracigaa aataccccca ccataccccc titoccctta. > 61 toacaaacta tgtggaatac tattgctact ccagaacaat gatctttagt taatctacac 65 totaggttaa ttgtatcate taattacett gcagacceta aaatcagaga agattgagtt 120 130 240 🕮 tyttqtaget cowlatgaag dagatgotoa gttagogtad atgtotoago ttggagtada 500 67 adatqqrqda qtiqcaqeqq tgatcacaga agataqtqat ctaataqcat atgqctqtcc > 69 agctgtaaga actcctccaa tactgtgata ttgcgcatgg aggtttactg qnnttttgat 360 71 a congatit atomacingt toachathea getheataga aageangean titiggganat 430 4:3 76 - 210: SEQ ID NO: 4 77 -0:110 LENGTH: 462 78 - B190 TYPE: DNA 79 - 2132 CEGANISM: G_ycine_max 81 -223> OTHER INFORMATION: unsure at all n locations E--> 82 <400> SEQUENCE: 4 84 icccatotgi tottiagoig tacaaaaaada caatooctat datggattaa cadatogaga

86 geattiteag deaacceaag geaceactic tigcaacaca ciaciggeet acacgdateg 120 88 aaacaqtaca geagaigaaa aiggigggic geattaacci teacaattig geageacaga 180

4 <1205 TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

60

1.50

RAW SEQUENCE LISTING PATE: 01/09/2003 PATENT APPLICATION: US/09/421,106A TIME: 10:55:57 light Set : D:\SoyBac.txt Output Set: N:\CRF4\01092003\I421106A.raw 90 äätinggadta tittiotuaaa ogaacoatti äätiggaagda qaatqaatga goatqoaqtgi. 240 300 92 ttactqqtct qqtcatqqtt cacaqaqctq qaqaaaaqat ttacaqaqca ttacaactac > 94 tggtccagca acctatcagt agctntctgt aactagcata gatgggaagc tattgaccaa 360 96 atglaacaut glatotugto tggattetaa cagagggano ticutoccan acagtnatac 420 463 98 tectquatto thagtacood agraettato tataatataa at 1(1 <21)> SEQ 1D NO: 5 102 <211> LENGTH: 394 10 5 K MAR FYPE: DNA 5/2201 ORGANISM: Glycine max 106 4328 OTHER INFORMATION: unsure at all n locations E--> 107 <400> SEQUENCE: 5 109 agetitecet etitgaacaa atabeeetea geeaaataga ateeatettg ggeettitte 11i chachaitet caraantggg agagaaatgt teatetaaag eatacaagte cetaatatta 113 toasatoreta asattigago tootagggag casaaraatg tgtgtntoot agagagggoa. 115 teacctacea carrigitit tecestitig tattigalaa caratggaaa tigetetagg 240 117 sacretacee attitiquatig constriggt aastigetit gecenetaat gractiaagt 119 participat cartaignat gacamattee tiggmearms getginging accordic 3611 ⊕ > 121 ngcgggaggg cgacgcgtga ctcgcgggat gcgt 394 184 - 210 - SEQ ID No: 6 13% <211% LENGTH: 464 116 TILL TYPE: DIM. 127 Hill F (EGANISH: Glycine max

129 KO23: OTHER IMPORMATION: unsure at all n locations E--> 130 <400> SEQUENCE: 6 🎢 > 132 ntaagaggat gctntaatgg agganaataa agagagaagg ngggagcaca aaattgaagg 114 hatsaastag ggagagaagt ggaacattga agtgtgtoto ataagacttt cattoatcaa

180 Tiff agtiaceans agrettacad atgettetat tiatagamia ggtagmitod tigagaagot 13% treifgagga sauttuettg agaaacttit tigaaaaaac ficetigaga aggtagaget 240 14% tagetarada cancestoto ataactaago teabetenti gagaagtitto cataagaaga 300 142 itertawaga agritagagit tagehabasa tabeteteta atagetawage teaceteett 300 144 gagatgggaa gctagagctn tgctacacac ccnctatgat agctaagctc acccccatga 420 146 caaaatacat ganaatacaa aaaagatccc tactacaaag acta 464 143 (210) SEQ 10 NO: 7 150 H211> LENGTH: 375 151 -212: TYPE: DMA. 182 02130 OEGANISM: Glycine max) 2 2 7 194 02230 OTHER INFORMATION: insure at all n locations



E--> 155 <400> SEQUENCE: 7 $\eta \sim$ 157 agetntgaaa agtgttgttn tteaeettet egetaageea ateegetgge ttagegageg 60 189 teogetsage genacactea tiggetaage geaaggaaga atetggaaga aaatgagetg 120 161 managettog oftageadad tigtificated cactaagege acceptitoag tecateaget 180 163 Hagdomadama godhacqoqot maqqoqamat tomotamiqt gogotamagog giocagamatt 240 16% regetaliging cargagolog alcaaggool octatitalig ottgalatol gattitigiga 300 350 167 agggagtttg ggctaggatt cagagetttg catgtetaga gattetagag agagaaaggt 373 169 ocaatttoag aga

136 -1210> SEQ ID NO: 9 197 -0211> LENGTH: 421 198 KL120 TYPE: DNA

199 K213> CEGANISM: Glycine max

RAW SEQUENCE LISTING

FATENT APPLICATION: US/09/421,106A

DATE: 01/09/2003 TIME: 10:55:57

input Set : D:\SoyBac.txt Output Set: N:\CRF4\01092003\I421106A.raw 201 <223 CIHER INFORMATION: unsure at all n locations E--> 202 <400> SEQUENCE: 9 204 agentitgadt itagteatoa agagattata aanatgigad aatggdatga gittidaataa 206 taateaataa tejateiitt acafäätet! etiteaacae eetteaatea atetticaat 20E atettettta atetetteea acattiteaa gagatettte tgatteattt coetteatet 240 210 tictaaaagt tiitoiteaa täyttietet teeaagaaaa gitetiitgit eaaaaaette 311 211 agetaticat citticatt eleticide filogogaaaa qaaggaagga claacegeet 360 214 gaattttttt gtgtctctct tctcccttac aaaagattca naggactaac cgcctgatat Nie afotittott toopoalada aagatitaaa ggadtaactg dotgagaatt crittgiooba. 4.214:1 215 a 2.5 <210> SEQ ID NO: 10 2. H <211> IENGIH: 404 Bur <2127 TYPE: DNA 2.54 K2131 CRGANISM: Clycine max) $\angle 2207$ z.+.<222) OTHER INFORMATION: unsure at all z locations E--> 227 <400> SEQUENCE: 10 2.10 tatofigeost coestiasca gracetical agraggigea ggaccaticaa cagebageeg 23. hagaigeace areacegost etacateage etergienti agagiseate trageicana. 1. 1 10 Pro tychonogat tyaseticat atycatysat atalysaana tytyysisgan saatayysyy 2 % graaf cating gogstaggtg cagetgaate agagettita eeagtacaee etaegteage $\mathbb{R}^{d_{i}}$ agagetagga theragedet tactogtgge thactodega gtagtttggg gedacagttg 2 + ratgoectig agutaggese aattiticaag tägggacaag accetsaaag geoosaggag Sec. 🦴 241 ttgaagatgg agctcaagaa gacgacgaca tangcgatgt gatg 404 G KING SEQ ID NO: 15 Calle LEMGTH: 359 * CRIZE TYPE: DNA 200 (215) CRGANISM: Glycine max \longrightarrow $\angle 2 2c 2$ 2 - 4 8 x 250 OTHER INFORMATION: unsure at all n locations En-> 290 <400> SEQUENCE: 13 24. agetigosto actititados titidatitido ategiadot ingolicadad actgoccado 2.4 originaging tilitagingt califattota atcaacatag iggatgatat igotocaaac 12 > 296 aagattgete ttgeetttga etttetetat eteetetegn gatttttttt atttgageaa T24- ocgi:gatta tecaptaggg giggaactic gialatgici itaalateti eesalagaic 240 -> 300 acaagcatca agatagggtt ccgttctaat agcctagagg tggtaatgtt ntccattgaa 300 2 . tagiquasago otaligaagoa oggacaccot agicoctia 3.7 kaio: **seg ib n**0: 15 3. 7 <2120 TYPE: DNA 340 k2130 GEGANISM: Glydine max \longrightarrow \angle 2 2 σ >3 : K223: OTHER INFORMATION: unsure at all n locations E--> 333 <400> SEQUENCE: 15 >, 335 agcttgcata actntgaatg gngtattggt agagtttatc cgttaatgat atgggctatt 60 337 gagttgggga ggattgattn tggaacttgt cgtggtgcag aagttagttc aagtgcgaac 120 150 3-+ actactagaa aanqaqettt tigegatgea ettaegaeat eggiceaaca aaactgiega 2:1 34: Agtafattsa atggigdatt tgtgtaatta daadgaaagt gigdassttg ddaattttät 300 34 - yyffigacatt gycsimaacto coffigaaggt fythygaagg gactogagag fyaggaaact 360 34- agadagetig gggtatteto gatttoogta adatäettaa tgetoteada adatagtigga

384

355 <210> SEQ ID NO: 13

:47 grtagggtag tadaitticac catt

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/421,106A

DATE: 01/09/2005 TIME: 10:55:57

Input Set : D:\SoyBac.txt

Output Set: N:\CRF4\01092003\I421106A.raw

```
289 - 2112 LENGTH: 442
       390 - 312: TYPE: DNA
       491 ≪135 CRGANISM: Glycine máx → ∠∠∠2o?
       593 42230 CTHER INFORMATION: unsure at all h locations
E--> 394 <400> SEQUENCE: 18
W--> 396 ctnggtgttg ttcctattgt gcgagttact gaggtgcaat ttcaatttta attggataat
       500 gagazatgit agcastalar tanogtalga cactgoatra bacactitat tattigonac
                                                                                                      120
      400 aastiastigs aantsamaan attiigigg tiotettami taittaatga acticastog
      40. Equititiqua athirialia aattitaaco aataataata ataatagagi gigitarita
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   -> 406 ccattttaaq tattatcctq taccanaacc tcactttaqt ccccaatttt ggaaatcaca
                                                                                                      360
W--> 408 gttcttttca ctgacaaatg acttacagtt ntagttaaaa atagggatta acaagagtgg
                                                                                                      420
                                                                                                      44.3
      410 agsatacang accasquigg act
      415 <2150 SRQ ID NO: 10
      414 <211% IENGTE: 396
      415 <2122 TYPE: DNA
      416 (213) TRUANISM: Glycine max \longrightarrow 22207
      415 (2.13) OTHER INFORMATION: unsure at all n locations
E--> 419 <400> SEQUENCE: 19
      401 agenttagent ggactaggaa äcuttataan eeetteaata ghaggatgag agtatgeete
                                                                                                     - 6 I
      41\% typingtärt tektionigt attytyllitä litetagaan aagaataaga gaadattaaa -12\%
      4.5 gg pantyskig tragton at garataliga gattigtill tittigtill tittigtaati. 185
     42\% gātsāassag schsastigg tigtotttitgi attaaggigd cittleagaag aacitigtigaa.
       4≯ aaraaatiga toagtifaat troottalad tidaaqigaa aagattittä taotaigaad
                                                                                                      21) 1
WH-> 431 taaccaaaaa tcatcctatg attnttaata taattattat aaaattacca tacatcataa 360
                                                                                                      396
W--> 433 tttgagaatg tagaanacat aaacaacgtt tacact
      456 <210% SEQ ID NO: .00
      437 42170 LENGTH: 469
      456 KRIED TYPE: DNA
      E--> 442 <400> SEQUENCE: 20

ho_{/}444 gtcctcgggc cattcctgcg aaggaaaaca tttggatagt tagttntacc aagaaatgct
    \mathcal{C}_{446} acceptisaga bahasan ged atacaacete etecaataaa tacaaacate aatgtaaatti
      44) tagadesage thatgograf attitudiae gaadattoad togdadaaga tattoticla.
      450 actiángadaa atquaccolat geacaateaa ggeaettteg ttacetaeat taittgiatg 240
      Idi tabirorang giqtaciado tabarbabat goattiboti gobiaaatti abatabatgo
      4/4 atom cases concerns to accase agent graduating search that g
                                                                                                     360
      45% gotia: ctada cantaaqqtg ctacactica tgotttatat caagtgitti actaccagaa.
                                                                                                     4000
      45% googratgog satgtomyta tattititit tigoogacta
                                                                                                      4 5 9
      461 <2100 SEQ ID NO: 111
      4 %: <211> LENGTH: 328
      493 KRIBO TYPE: DNA
      464 <213> OEĞANISM: 6.ycine max _
      466 <223> OTHER INFOFMATION: unsure at all n locations
E--> 467 <400> SEQUENCE: 21
      469 agettriced coalitited atalataggg ggagaagtgt agtagalaag ggttcagtro
      471\ \mathrm{cttaggeact} interest togaattige staggoaaat ightice\mathfrak{g}\mathfrak{t}\mathfrak{g} aagaaaatee
      475 aageogagge getteegtaa egttteegtg ägtgatttig egaaggittit egaeegitet
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DATE: 01/09/2063

TIME: 10:55:57 FATENT APPLICATION: US/09/421,106A Input Set : D:\SoyBac.txt Cut put Set: N:\CRF4\01092003\I421106A.raw W--> 475 tegaegntet teattegtte tteategnte tteagtette aaegggtaag taceteatae \mathbb{W}_{r} > 477 caagetttte aatteattet atataeeegn nnggggeeae attatggtte atgtattatt 479 attetegntt catttactet ttatacce 328 48.1 <210° SED ID NO: 32 483 <211 - LEUGTH: 391 404 < 12 TYPE: DNA 4-5 K:13 OP ANISM: 3. veine max \rightarrow 22 207 4m: <.:23 OTHER INFORMATION: unsure at all m locations E--> 488 <400> SEQUENCE: 22 1/7/> 490 ggctctanat ntacattgat gtttgtattt atgggaggag gttatatgcc atttttgctt 4.6 taagagtaso gtorramingg taaaantaac tttccaaatg titigccticg caggaatgdc 120 499 dingagasy officializational agaggionag gaaggabaag geggongaag gaactagite 106 ogeo-caing tackshipto acceptitiag gagegtigta cascageage gottogaage 499 gatrwaggia tygtoposto toogugagog acgogtocag otoatggaog abgagtätac 500 trastitorig gaqiasilaq gguqonqqeq qtqqqbacca ttqqttactb chatqqnbaa 367 501 jittaatera gaaatajind tigagiitta i 391 5. 5 9. 10 SEP ID NO: 24 5. 6 K. 11 DENGCH: 488 % TR. 12 IYFE: DNA 5.8 < 13 - OFBANISM: Drycine max 2227 6.0 0.23 OTHER INFORMATION: unsure at all n locations E--> 531 <400> SEQUENCE: 24 🟃 533 ggcacactot ntgattatot tggtotacca agtgtttatt acacaatagt gaaatgcact tesbotarinocari ofocavigeto asperentara tegaattato tocagocaco caretacano 1.20 ~ 7 пывыяварыў ўtтызыяваў ўваўсчынаст ласлостусся афалосская ўtt chayyt tFirst tragetigges attracts that takeassang ggttotacas cotottatag asgestaach 54. Stiplassha otritsutag täsamusgää ämaaaaaact itasgicaca gäänisanta [43] o sautqăua aactar mac attgliiqqtt tgtactetge agtotgeaeg tgttteeata. 560 145 aasadaaana cartganiitti aaattaatta atrgattaat actaocatca agtagtacca. 4.20 14% draggatant othitetha 4 35 5 -4 -4, 146 SEG 10 NO: 27 185 K. 11 - LENGTH: 373 * MG C 12 - TYPE: DNA FOR CLIB CEMANISM: Phycine max $\frac{2207}{1.00}$ E--> 590 <400> SEQUENCE: 27 W--> 592 agettetece ecaattntet ataaataggt ggagaagtga agtgaanaag ggtteageee industrial agreement that the state of the second s 1:20 E-W asgeogagic gentrogaaa egitteegia aegitteegi gaggaatite gegaaggitt 180 -240Note: these square caughtitie gatteattet atgtacetgt ggtggtecae attgtggtte 3.00 360 W--> 602 gtggattttt attotogntt catttacttt ctataccccc ttttgacgtg gottaagcca + F4 ittätttaag toatitoid 379 +19 < 100 SEQ ID NO: 29

RAW SEQUENCE LISTING

E--> 635 <400> SEQUENCE: 29

6 2 < 13> ORGANISM: G.ycine max___) < 2207

654 < 23> OTHER INFCEMATION: unsure at all n locations

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/421,106A

DATE: 01/09/2003 TIME: 10:55:57

lnput fet : D:\SoyBac.txt

Output Set: N:\CRF4\01092003\I421106A.raw

W-,->					ttaaccccat			60		
~{\ W }/ ₇ >					caacccanaa			120		
W>	641	ntatctatga	actgtacaaa	atacacgact	cctcaattgt	tctcaaaata	attttatcta	180		
	64?	atogogotty	tgättaaant	lågt daggt de	caacagtiggt	toccatoata	atactogoda	240		
	54€	egeattaact	agtagecet t	agatteatag	ticacaaato	agggcacaca	acaticticaat	500		
	647	gcacatătat	attacaaqto	aatacatadt	caatttatca	catacattig	gtotcaatca	360		
	649	gagtggtata	atctcaattt	aacatgttat	cacacctcat	gaatsata		4 O E		
	652	<2100 SEQ 0	ID 110: 30							
		<211: LENGT								
		<212. TYPE:								
			NISM: Glycin							
		<pre><223: OTHER INFORMATION: unsure at all n locations</pre>								
		<400> SEQUE								
Wr->					acaagattac			60		
					aaatcatgag			120		
$I \setminus I$	664	ttaadgttat	ageläääaaadg	gtitcagcta	aaasaaat gc	aaggsagcgt	aagaaataaa	180		
116					tacataaaca			240		
		-			atgetgttte			306		
()				• *	aagtcataaa	_		360		
W>		-			taattntaca	ccctccccan	acccacaatg	420		
			aaqqaataca	icq				443		
		<810: SEQ 1						_		
		<211: LENGT								
		<pre><212</pre>		i	155					
	985	<.215.1 UKGAI	NISM: Giyali	· max		+				
				n: unsure a	at all n'loc	gations		\		
E>		<400> SEQUI		** ** * * * * * * * * * * * * * * * *	t 222224ttt	not contitue	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 	€) Î	\	
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16 ×					ctggacctag			300	/	
-100					agetecaaça			360 /		
(-			ttacgtgaat			cegeagegee	aggsecancg	398		
	057	ceaceaagee	ccasgegaac	ggcccccccc	acagecae					
						,				
						/				
						(-			

MI

see p.7 for more orion

09/421,106A 7

<210> <211> <212> <213>	36937 22 DNA Artificial Sequence
<400>	36937 Leg gatgettett et leg 22
gtgtcttt	teg gatgettett et
<210>	36938
<211>	22
<212>	DNA
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caccattttg cacctaagtt ga



PATE: 01/09/2003 TIME: 10:57:26

RAW SEQUENCE LISTING ERROR SUMMARY LATENT APPLICATION: US/09/421,106A

Inplut Set : D:\SoyBac.txt

Output Set: N:\CRF4\01092003\I421106A.raw

Use of <220> Feature(NEW RULES):

Sequence(s) _are missing the <220> Feature and associated headings. Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32) (Sec.1.823 of new Rules)

Seq#:36937,36958